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Minimum
Maximum
                                                                                                                                                                                                                                      Result
                                                                                                                                                                                                                                                                                                                             Database
                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 10
Listing first 45
                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
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Perfect score:
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1: pir1:*
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Gapop 10.0 ,
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342
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2001, 15:52:41; Search time 170.72 Seconds (without alignments)
23.864 Million cell updates/sec
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       protein
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RESULT 1 S22477 Vicilin precursor - cacao (cacao) C; Species: Theobroma cacao (cacao) C; Onte: 30-Sep-1993 #sequence_revision C; Accession: S22477; S22478; S18105; S; R; McHenry, L.; Fritz, P.J. Plant Mol. Biol. 18, 1173-1176, 1992 A; Title: Comparison of the structure at A; Reference number: S22477; MUID:92288, A; Accession: S22477 A; Molecule type: DNA A; Residues: 1-566 <mch> A; Residues: 1-566 <mch> A; Residues: 1-566 <mch> A; Cross-references: EMBL:X62625 A; Cross-references: EMBL:X62625 A; Cross-references: EMBL:X62626 C; Genetics: 1-452 <mc2> A; Cross-references: EMBL:X6263; 391/3; C; Superfamily: glycinin C; Keywords: seed: storage protein F;1-24/Domain: signal sequence #status F; 25-566/Product: vicilin #status predi</mc2></mch></mch></mch>	4444444 544444 544444 54444 5444 5444
SULT 1 24477 Cilin precursor - Cilin precursor - Species: Theobrom Date: 30-Sep-1993 Accession: S22477 MCHenry, L.; Frit: Ant Mol. Biol. 18 Title: Comparison Reference number: Accession: S22478 Molecule type: DNN Molecule type: DNN Molecule type: DNN Cross-references: Accession: S22478 Molecule type: MRR Residues: 1-56 Cross-references: Accession: S22478 Molecule type: mRR Title: Cross-references: Genetics: 1-452 Cross-references: 1-452 Cross-references: 1-452 Residues: 1-452 Residues: 1-452 Residues: 1-452 Cross-references: Superfamily: 9171; 21 S	84.5 83.5 83.5 83.5 83.5 83.5 83.5 83.5 83
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<pre>#text_change 17-Mar-1999 s sequence of vicilin genes of coco</pre>	protein kinase (EC hypothetical prote involucrin L - dou hypothetical prote androgen receptor regulatory protein stripe a/b protein involucrin - mouse trfA protein - sli multidrug resistan ALR protein - huma ALR protein - huma transcription init vicilin-like stora hypothetical prote gap protein hunchb

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RESULT 2
$08059
Solution type B precursor (tandem 1) - upland cotton (fragment)
N;Alternate names: seed storage protein
C;Species: Gossypium hirsutum (upland cotton)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-Sep-1993
C;Accession: $08059
R;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.
Plant Mol. Biol. 9, 533-546, 1987
A;Title: Developmental biochemistry of cottonseed embryogenesis and germinal A;Reference number: $06398
A;Accession: $08059
A;Accession: $08059
A:Status: not compared with conceptual translation A:Molecule type: DNA A:Residues: 1-509 <CHL>
C:Superfamily: glycinin
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Pred. No. 1.3e-25;
; Mismatches 0;
                                                                                                                              cottonseed embryogenesis and germination. XIX.
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C;Superfamily: glycinin
C;Keywords: glycoprotein; seed; storage protein
E;1-25/Domain: signal sequence #status predicted <SIG>
E;26-588/Product: alpha-globulin storage proprotein #status predicted
E;417/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alpha-globulin B precursor (clone C72) - upland cotton
N;Alternate names: seed storage protein; vicilin precursor
C;Species: Gossypium hirsutum (upland cotton)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C;Accession: A30838; S06911
R;Chlan, C.A.; Pyle, J.B.; Legocki, A.B.; Dure III, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-605 <CHL>
A;Residues: 1-605 <CHL>
C:Superfamily: glycinin
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-605/Product: alpha-globulin type A #status predicted <MAT>
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C;Species: Gossypium hirsutum (upland cotton)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-Sep-1993
C;Accession: S06398
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                                                                                                                              C; Comment: This is a seed storage protein
                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-81 <CH2>
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                                                                                                                                                                                                                                   A; Reference number: S06398
A; Accession: S06911
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A;Experimental source: var. Coker 201
R;Chlan, C.A.; Borroto, K.; Kamalay, J.A.; Dure III, L.
Plant Mol. Biol. 9, 533-546, 1987
                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-588 < CHL>
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A;Title: Developmental biochemistry of cottonseed embryogenesis and germination
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A; Accession: S06398
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                                                                                                                                                                                                                                                                                  A; Title: Developmental biochemistry of cottonseed embryogenesis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: A30838
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Best Local Similarity 43.3
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9, 1986
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Pred. No. le-05;
12; Mismatches
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Pred. No. 1.2e-05;
4; Mismatches 18
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R:Rieben Jr., W.K.; Gonzales, C.M.; Gonzales, S.T.; Pilkington, K.J.; Kiyosawa, H.; H Genetics 148, 1117-1125, 1998
A:Title: Dictyostelium discoideum nuclear plasmid Ddp5 is a chimera related to the Dd A:Reference number: Z14684; MUID:98198836
A:Accession: T02634
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C:Species: Cucurbita maxima (winter squash)
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
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                                                                                                                                                                                         A; Genome: plasmid
A; Mobile element:
                                                                                                                                                                                                                                     A;Gene: rep
                                                                                                                                                                                                                                                           C; Genetics:
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                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-1038 < RIE>
                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: T02634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rep protein homolog - slime mold (Dictyostellum discoideum) plasmid
C;Species: Dictyostellum discoideum
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 29-0
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A; Residues: 1-810 < YAM>
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A;Title: Multiple functional proteins are produced A;Reference number: Z22767; MUID:99107919
A;Accession: T44430
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Best Local Similarity
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Best Local Similarity 31.6
Matches 18; Conservative
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Best Local
940 QEQQEQRERREQQEQQEQQEQQE-QQEQQEQQEQQEQQEQQEQQEQQEQREQEEQEEQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 QRQFQECQQHCHQQEQRPERKQQCVRECRERYQENPWRREREEEAEEEETEEGEQEQSHN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity hes 29; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 EYEVCRLRCQVAERGVEQQRKCEQVCEERLREREQGRGEDVDEVERRDPEWEREEQR 133
                                  2 QRQYQQCQGRCQEQQQGQREQQQCQRKCWEQYKEQERGEHENYHNHKKNRSEEEEGQQR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 QYQQCQGRCQEQQQGQREQQQCQRKCWEQYKEQERGEHENYHNHKKNRSEEEEGQQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFHFHRRSFQSRFREEHGNFK 201
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                                                                                     Conservative
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                                                                                                                                                                                         plasmid
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                                                                                                      30.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 104; DB 2; Pred. No. 0.0088;
                                                                                Score 103.5; DB Pred. No. 0.012; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 132; DB 1; Pred. No. 1.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M.; Nishimura, M.; Hara-Nishimura, I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                            Length 1038;
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RESULT 8
A53185
G-box-binding factor - slime mold (Dictyostellum discoideum)
C;Species: Dictyostellum discoideum
C;Species: Dictyostellum discoideum
C;Species: O6.Jan-1995 #sequence_revision O6-Jan-1995 #text_change 24-Sep-1999
C;Accession A53185
R;Schnitzler, G.R.; Fischer, W.H.; Firtel, R.A.
Genes Dev. 8, 502-514, 1994
A;Title: Cloning and characterization of the G-box binding factor, an essenti A;Reference number: A53185; MUID:94170994
A;Accession: A53185
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-708 <SCH>
A;Cross-references: GB:L29075; NID:9456561; PIDN:AAA21021.1; PID:g456562
C;Superfamily: G-box binding factor
C;Keywords: DNA binding; transcription factor; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Desansky, N.J.; Paskewitz, S.M.; Mills-Hamm, D.M.; Collins, F.H. submitted to the EMBL Data Library, June 1992
A; Description: Distinct families of site-specific retroposons occupy identical positions A; Reference number: $27770
A; Recession: $27770
A:Cross-references: EMBL:AL050398; GSPDB:GN00062; ATSP:L23H3.30 A:Experimental source: cultivar Columbia; BAC clone L23H3 C:Genetics: A;Gene: ATSP:L23H3.30 A:Map position: 4
                                                                                                        R:Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; submitted to the Protein Sequence Database, May 1999 A;Reference number: Z16098 A;Accession: T08588 A;Molecule type: DNA A;Residues: 1-930 <BEV>
                                                                                                                                                                                                                   hypothetical protein L23H3.30 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 11-Jun-1999 *sequence_revision 11-Jun-1999 *text_change 22-Oct-1999 C:Accession: T08588 R;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein 1 - African malaria mosquito (fragment) (Speciles: Anopheles gambiae (African malaria mosquito) (C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Sep-1997 C;Accession: S27770 R;Besansky, N.J.; Paskewitz, S.M.; Mills-Hamm, D.M.; Collins, F.H.
                                                                                                                                                                                                                                                                                                                                  T08588
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A; Residues: 1-613 <BES>
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Best Local Similarity 31.3
Conservative
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Pred. No. 0.08
14; Mismatches
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Pred. No. 0.017;
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0.087;
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A;Gene: yakA C;Keywords: ATP; phosphoprotein; phosphotransferase;
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A;Molecule type: mRNA
A;Residues: 1-1457 <KUS>
                                                                                                                                                                                                                                                                                                               A; Reference number: A; Accession: T14577
                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, January 1998 A; Description: YakA, a protein kinase required for A; Reference number: Z18146
                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                 protein kinase YakA (EC 2.7.1.-) - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1
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T14577
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A;Title: DNA sequences homologous to the Drosophila A;Reference number: A26892; MUID:87257908
A;Accession: A26892
RESULT
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                                                                                                                                                                                                                                            A;Cross-references: EMBL:AF045453; NID:g2854116; PID:g2854117; PIDN:AAC02554.1
                                                                                                                                                                                                                                                                                                                                                                                R; Kuspa, A.; Lu, S.; Souza, G.M.
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C;Accession: A26892
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A26892
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A; Residues: 1-139 < DUB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Species:
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                                                                                                              Query Match
Best Local Similarity
Matches 17; Conser
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Best Local
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ecies: Mus musculus (house mouse)
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27.9%;
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Pred. No.
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Pred. No.
                                                                                                                               Score 91;
Pred. No.
                                                - OQQQQQQQQQQQQHNQFQQQQQQQQQQQQQ
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0.027;
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                                                                                                                                              DB 2;
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dog

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R:Gubbay, J.; Collignon, J.; Koopman, P.; Capel, B.; Economou, A.; Muensterberg, Nature 346, 245-250, 1990
A:Title: A gene mapping to the sex-determining region of the mouse Y chromosome A;Reference number: S10938; MUID:90326154
A;Accession: S10938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-285 <TSE>
A; Residues: 1-285 <TSE>
A; Cross references: GB: M34442; NID: g163980; PIDN: AAA30853.1; PID: g163981
C; Comment: During the terminal differentiation of keratinocytes, this protein linked envelope under the plasma membrane.
C; Superfamily: involucrin
C; Keywords: cornified cell envelope; duplication; epidermis; tandem repeat
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                                                                                                                                           QΥ
                                                                                                                                                                                                                                                                                                                                         C;Superfamily: unassigned HMG box proteins; HMG box homology C;Keywords: DNA binding; nucleus; sex-specific protein; transcription regulation F;2-77/Domain: HMG box homology <HMG1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sex-determining protein SRY - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Jan-2000
C;Accession: S35565; S10938; A59162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Biol. Evol. 7, 293-302, 1990
A;Title: The involucrin genes of pig and dog: comparison of their segments of A;Reference number: 146207; MUID:90348475
A;Accession: 146207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: I46207
R; Tseng, H.; Green, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Canis lupus familiaris (dog)
C;Date: 16-Aug-1996 #sequence_revision 23-Aug-1996 #text_change 22-Jun-1999
C;Accession: I46207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:X55491; NID:g287804; PIDN:CAA39111.1; PID:g287805
A;Note: the sequence is revised in GenBank entry MMSRVA, release 113.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-125 <GUB>
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A;Accession: A59162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Tucker, P.K.; Lundrigan, B.L. Nature 364, 715-717, 1993
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A; Residues: 'TGDNCLES', 1-91 <MOU>
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A; Residues: 1-395 < TUC>
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Best Local
                                                                                    160 QQQQQFYDHHQQQQQQQQQQQQFHDHHQQKQQFHDHHQQQQQQFHDHHHHHQEQQFHDHHQ 215
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Similarity 28.6%;
18; Conservative :
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Pred. No. 0.069;
                                                                                                                                                                                                Score 90.5; DB 2;
Pred. No. 0.091;
0; Mismatches 20;
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                                                                                                                                     A;Cross-references: EMBL:X76053; NID:g600025; PIDN:CAA53652.1; PID:g429134 R;Brandt, T.; Christiansen, C.; Holmstroem, K.; Kallesoe, T. submitted to the Protein Sequence Database, August 1994 A;Reference number: S46157 A;Reference number: S46157
                                                                                                                                                                                                                                                                                                                                                                   C;Date: 30-Sep-1991 #sequence_revision 09-Sep-1994 #text_change 21-Jul-2000 C;Accession: S44551; S46171; A36375; S12067; S39145 R;Holmstrom, K.; Brandt, T.; Kallesoe, T. Yeast 10(Suppl.A), S47-S62, 1994 R;Title: The sequence of a 32420 bp segment located on the right arm of chr. A;Reference number: S44537; MUID:94378722 A;Accession: S44551
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R;Coward, P.; Nagai, K.; Chen, D.; Thomas, H.D.; Nagamine, C.M.; Lau, Y.F.
submitted to the EMBL Data Library, November 1993
A;Description: Polymorphism of a CAG trinucleotide repeat within Sry corre
A;Reference number: S78062
A;Accession: S78062
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A;Title: Polymorphism of a CAG trinucleotide repeat within Sry correlates with B6.Y(D A;Reference number: S43344; MUID:94282071
A;Accession: S43344
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C:Species: Mus musculus domesticus (western European house mouse)
C:Date: 25-Dec-1994 #sequence_revision 03-Nov-1995 #text_change 2
A;Cross-references: EMBL:236158; NID:g536741; PIDN:CAA85254.1; PID:g536742; GSPDB:GNO R;Laurent, B.C.; Treitel, M.A.; Carlson, M. Mol. Cell. Biol. 10, 5616-5625, 1990
                                                                                 A; Residues: 1-905 < BRA>
                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-905 <HOL>
                                                                                                                                                                                                                                                                                                                                         A; Status: translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Species: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             regulatory protein SNF5 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YBR2036; protein YBR289w
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C;Keywords: DNA binding
F;2-77/Domain: HMG box homology <HMGl>
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A; Residues: 1-395 < COW>
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Best Local
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A.Title: The SNF5 protein of Saccharomyces cerevisiae is a glutamine- and proline-rich A:Reference number: A36375; MUID:91042489
A:Accession: A36375
A:Molecule type: DNA
A:Residues: 1-563, 'D', 565-905 < LAU>
A:Cross references: GB:M36482; NID:9172637: PIDN:AAA35062.1; PID:9172638
C;Genetics: A;Gene: SGD:SNF5; MIPS:YBR289w
A;Cross references: GB:M36482; NID:9172637: PIDN:AAA35062.1; PID:9172638
A;Cross references: SGD:S0000493; MIPS:YBR289w
A;Cross references: SGD:S0000493; MIPS:YBR289w
A;Cross references: SGD:S0000493; MIPS:YBR289w
A;Cross references: SGD:S00000493; MIPS:YBR289w
A;Cross references: SGD:M36482; MID:9172637: PIDN:AAA35062.1; PID:9172638
A;Cross references: SGD:M36482; MID
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